



SEQUENCE LISTING

<110> PLOWMAN, GREGORY D.  
WHYTE, DAVID  
MARTINEZ, RICARDO  
HILL, RONALD  
FLANAGAN, PETER  
LIOUBIN, MARIO

<120> NOVEL PROTEIN PHOSPHATASES AND DIAGNOSIS AND TREATMENT  
OF PHOSPHATASE-RELATED DISORDERS

<130> 034536-0726

<140> 10/049,515

<141> 2002-06-14

<150> PCT/US00/22158

<151> 2000-08-11

<160> 45

<170> PatentIn Ver. 3.2

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Asp Phe Cys Pro Pro Ser Pro Glu Gln Ile Asp Gln Phe Val Lys Ile  
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Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala  
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Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys  
100 105 110

Glu Arg Ala Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu  
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Phe Tyr Gln Arg Thr Lys  
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 35 40 45

Gly Pro Arg Ala Pro Gly Val Ala Glu Leu Arg Val Pro Val Phe Asp  
 50 55 60

Asp Pro Ala Glu Asp Leu Leu Thr His Leu Glu Pro Thr Cys Ala Ala  
 65 70 75 80

Met Glu Ala Ala Val Arg Asp Gly Gly Ser Cys Leu Val Tyr Cys Lys  
 85 90 95

Asn Gly Arg Ser Arg Ser Ala Ala Val Cys Thr Ala Tyr Leu Met Arg  
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His Arg Gly His Ser Leu Asp Arg Ala Phe Gln Met Val Lys Ser Ala  
 115 120 125

Arg Pro Val Ala Glu Pro Asn Leu Gly Phe Trp Ala Gln Leu Gln Lys  
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 Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val  
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Glu Thr Trp Glu Asp Ala Thr Val His Val Val Glu Thr Glu Pro Ser
          35              40              45

Gly Gly Gly Gly Cys Gly Tyr Val Gln Asp Leu Thr Leu Asp Leu Gln
  50              55              60

Val Gly Val Ile Lys Pro Trp Leu Leu Leu Gly Ser Gln Asp Ala Ala
  65              70              75              80

His Asp Leu Glu Leu Leu Arg Lys His Lys Val Thr His Ile Leu Asn
          85              90              95

Val Ala Tyr Gly Val Glu Asn Ala Phe Leu Ser Glu Phe Thr Tyr Lys
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Thr Ile Ser Ile Leu Asp Val Pro Glu Thr Asn Ile Leu Ser Tyr Phe
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Pro Glu Cys Phe Glu Phe Ile Glu Gln Ala Lys Leu Lys Asp Gly Val
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Val Leu Val His Cys Asn Ala Gly Val Ser Arg Ala Ala Ala Ile Val
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Ile Gly Phe Leu Met Ser Ser Glu Glu Ala Thr Phe Thr Thr Ala Leu
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Ser Leu Val Lys Glu Ala Arg Pro Ser Ile Cys Pro Asn Pro Gly Phe
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 35 40 45  
 Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Gln Asn Leu Thr  
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Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg  
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Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val  
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Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu  
100 105 110

Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn  
115 120 125

Val Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His  
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Gln Tyr Arg Gln Trp Leu Lys Glu Glu Tyr Gly Glu Ser Pro Leu Gln  
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cagaaaaatgc aggcgggtctt tatttagaca ttctagtatt ttgggtcata gtgaaggaag 720
tgggccaata gcctttgctc acaagagaac ggcgccatct tctgtactta ccacagggag 780
tcaggctcag tgcacgtctt acttcattga gcctgtgcag tggatggaat ctactctgtt 840
gggcgttatg gatggacagc ttctttgccc aaaatgcagt gccaaagtgg gttcctttta 900
ctggtatggt gaacagtgtc cgtgtggtcg atggataacc cctgcttttc aaatacacia 960
gaacagagtg gatgaaatga aaatggtgcc ggcgctgggt tcacagacaa agaagctgtg 1020
aacttaggac ccagcttggg ctagatcctg tgaaaggcac ttccccgttg tcatcattca 1080
tggcggatgt caaacttctt ttggaatgtc cgaagacaat tactgactgt aacagctgtg 1140
ggttggtagc ttattatgtg gcataatatac agttacgttg cttggcaatt cagatattta 1200
gttatgtaag ttggatttgt tattaataac c          1241

```

&lt;210&gt; 16

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 16

```

Met Leu Glu Ala Gln Gly Thr Asn His Gly Cys Glu Arg Gln Ala Pro
  1              5              10              15

Thr Ala Ser Pro Ala Ser Ser Ala Gly His Ala Val Glu Val Arg Pro
              20              25              30

Gly Leu Tyr Leu Gly Gly Ala Ala Ala Val Ala Glu Pro Gly His Leu
              35              40              45

Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Pro Ala
              50              55              60

Phe Pro Ala Gly Ala Gly Phe Glu Gly Leu Arg Ser Leu Phe Val Pro
              65              70              75              80

Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg Cys
              85              90              95

Val Ala Phe Ile Gly Gln Ala Arg Ser Glu Gly Arg Ala Val Leu Val
              100              105              110

His Cys His Ala Gly Val Ser Arg Ser Val Ala Val Val Met Ala Phe
              115              120              125

Ile Met Lys Thr Asp Gln Leu Thr Phe Glu Lys Ala Tyr Asp Ile Leu
              130              135              140

Arg Thr Val Lys Pro Glu Ala Lys Val Asn Glu Gly Phe Glu Trp Gln
              145              150              155              160

Leu Lys Leu Tyr Glu Ala Met Gly Tyr Glu Val Asp Thr Ser Ser Ala
              165              170              175

Phe Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro Glu
              180              185              190

Leu Trp Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr Ile
              195              200              205

```

Ser Gln Gly Leu Lys Asp Asp Ile Leu Tyr Lys Cys Arg Lys Cys Arg  
 210 215 220  
 Arg Ser Leu Phe Arg His Ser Ser Ile Leu Gly His Ser Glu Gly Ser  
 225 230 235 240  
 Gly Pro Ile Ala Phe Ala His Lys Arg Thr Ala Pro Ser Ser Val Leu  
 245 250 255  
 Thr Thr Gly Ser Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro Val  
 260 265 270  
 Gln Trp Met Glu Ser Thr Leu Leu Gly Val Met Asp Gly Gln Leu Leu  
 275 280 285  
 Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly Glu  
 290 295 300  
 Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His Lys  
 305 310 315 320  
 Asn Arg Val Asp Glu Met Lys Met Leu Pro Ala Leu Gly Ser Gln Thr  
 325 330 335

Lys Lys Leu

<210> 17  
 <211> 904  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 gtgttccgct caggcagagt cctgccccctg caccactcc cccattcccg gccccaggcc 60  
 atgccccagg atggactcac tgcagaagca ggacctccgg aggccaaga tccatggggc 120  
 agtccaggca tctccctacc agccgcccac attggcttcg ctgcagcgct tgctgtgggt 180  
 ccgtcaggct gccacactga accatatcga tgaggtctgg ccagcctct tccctgggaga 240  
 tgcgtacgca gcccgggaca agagcaagct gatccagctg ggaatcacc acgttgtgaa 300  
 tgccgctgca ggcaagttcc aggtggacac aggtgccaaa ttctaccgtg gaatgtccct 360  
 ggagtactat ggcatagagg cggacgacaa ccccttcttc gacctcagtg tctactttct 420  
 gcctgttgct cgatacatcc gagctgccct cagtgttccc caaggccgcg tgctggtaca 480  
 ctgtgccatg ggggtaagcc gctctgccac acttgctctg gccttcctca tgatctatga 540  
 gaacatgacg ctggtagagg ccatccagac ggtgcaggcc caccgcaata tctgccctaa 600  
 ctcaggcttc ctccggcagc tccaggttct ggacaaccga ctggggcggg agacggggcg 660  
 gttctgatct ggcaggcagc caggatccct gacccttggc ccaacccac cagcctggcc 720  
 ctgggaacag caggctctgc tgtttctagt gaccctgaga tgtaaacagc aagtgggggc 780  
 tgaggcagag gcagggatag ctgggtggtg acctcttagc ggggtggattt ccctgaccca 840  
 attcagagat tctttatgca aaagttagtt cagtccatct ctataataaa atattcatcg 900  
 tcat 904

<210> 18  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 18

Met Asp Ser Leu Gln Lys Gln Asp Leu Arg Arg Pro Lys Ile His Gly  
 1 5 10 15

Ala Val Gln Ala Ser Pro Tyr Gln Pro Pro Thr Leu Ala Ser Leu Gln  
 20 25 30

Arg Leu Leu Trp Val Arg Gln Ala Ala Thr Leu Asn His Ile Asp Glu  
 35 40 45

Val Trp Pro Ser Leu Phe Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys  
 50 55 60

Ser Lys Leu Ile Gln Leu Gly Ile Thr His Val Val Asn Ala Ala Ala  
 65 70 75 80

Gly Lys Phe Gln Val Asp Thr Gly Ala Lys Phe Tyr Arg Gly Met Ser  
 85 90 95

Leu Glu Tyr Tyr Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu  
 100 105 110

Ser Val Tyr Phe Leu Pro Val Ala Arg Tyr Ile Arg Ala Ala Leu Ser  
 115 120 125

Val Pro Gln Gly Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg  
 130 135 140

Ser Ala Thr Leu Val Leu Ala Phe Leu Met Ile Tyr Glu Asn Met Thr  
 145 150 155 160

Leu Val Glu Ala Ile Gln Thr Val Gln Ala His Arg Asn Ile Cys Pro  
 165 170 175

Asn Ser Gly Phe Leu Arg Gln Leu Gln Val Leu Asp Asn Arg Leu Gly  
 180 185 190

Arg Glu Thr Gly Arg Phe  
 195

&lt;210&gt; 19

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

gtgagaggag acagaaagag ggtggtggcc gatagctggt cctctttctc caacacctag 60  
 cctgagactt ggcggcgcgg ctgctatcct gaactagctt ggtaagtgtt gtgtcccgaa 120  
 ccagcgtaga gagacctcgg accagccgcc ttgatgacag catccgcgtc ctctttttca 180  
 tcatctcagg gtgtccagca gccctccatc tacagcttct cccaaataac cagaagcttg 240  
 tttctcagca atggtgtggc cgccaacgac aaactccttc tgtccagcaa tcgcatcacc 300  
 gccattgtca atgcctcggg ggaagtgggc aacgtattct tcgagggcat tcagtacata 360  
 aaggtgcctg ttaccgatgc tcgtgactcg cgtctctacg acttttttga cccatttgct 420  
 gatcttatcc acaccatcga tatgaggcag ggccgtacgc tgctgcactg catggctgga 480  
 gtgagcgggt ccgcctcact gtgccttgcg tacctcatga aataccactc catgtcgctg 540  
 ctggagcggc atacatggac caagtcgcgc cgccccatca tccggcccaa caacggcttt 600  
 tgggaacagc tcatcaatta cgaattcaag ctgtttaata acaacaccgt gcgcatgatc 660

```

aactcgccgg taggtaacat ccctgacatc tatgagaagg acctacgtat gatgatatca 720
atgtaagcca tcccggccag ccctgacat, ctgccatcga tcttgacca agactgaact 780
ttgaacactg acattttgtt agtaaagaaa accggatggt gccttgtaa agggcaagaa 840
aaaagggagg gggttggagt tttgaacgta gtaagcctta ccttaataga attaaattca 900
tgaaacat                                     908

```

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<210> 20
<211> 190
<212> PRT
<213> Homo sapiens

```

```

<400> 20
Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln
  1              5              10              15

Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser
      20              25              30

Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile
      35              40              45

Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu
      50              55              60

Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg
      65              70              75              80

Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp
      85              90              95

Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg
      100             105             110

Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser
      115             120             125

Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg
      130             135             140

Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu
      145             150             155             160

Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile
      165             170             175

Pro Asp Ile Tyr Glu Lys Asp Leu Arg Met Met Ile Ser Met
      180             185             190

```

```

<210> 21
<211> 775
<212> DNA
<213> Homo sapiens

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```

<400> 21
aattacttag cggcgactga gcctatcgag cagttttcca tggacacagc ctagcagaaa 60
gacgcagcct tcgtgcttcg ctgactgctg accactgacc caccgccttg atgacagcac 120

```

```

cctcgtgtgc cttcccagtt cagttccggc agccctcagt cagcggcctc tcgcagataa 180
ccaaaagcct gtatatcagc aatgggtgtgg ccgccaacaa caagctcatg ctgtctagca 240
accagatcac catggtcatc aatgtctcag tggaggtagt gaacaccttg tatgaggata 300
tccagtacat gcaggtaacct gtggtgact cccctaactc acgtctctgt gacttctttg 360
accctattgc tgaccatata cacagcgtgg agatgaagca gggccgtact ttgctgcact 420
gtgctgctgg tgtgagccgc tcagctgccc tgtgcctcgc ctacctcatg aagtaccacg 480
ccatgtccct gctggacgcc cacacgtgga ccaagtcag cccgcccatac atccgaccca 540
acagcgggctt ttgggagcag ctcatccact atgagttcca attgtttggc aagaacactg 600
tgcacatggt cagttcccca gtgggaatga tccctgacat ctatgagaag gaagtccggt 660
tgatgattcc actgtgagcc atcccacgag cccctgcatt ggagtcagag gtacagatct 720
attgttgatc ttacaccaag atccaaactt gaacattcta cttttgttga tacag 775

```

<210> 22

<211> 188

<212> PRT

<213> Homo sapiens

<400> 22

```

Met Thr Ala Pro Ser Cys Ala Phe Pro Val Gln Phe Arg Gln Pro Ser
  1                      5                      10                      15

```

```

Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser Asn Gly
      20                      25                      30

```

```

Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile Thr Met
      35                      40                      45

```

```

Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile
      50                      55                      60

```

```

Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys
      65                      70                      75                      80

```

```

Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu Met Lys
      85                      90                      95

```

```

Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
      100                      105                      110

```

```

Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu
      115                      120                      125

```

```

Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
      130                      135                      140

```

```

Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly
      145                      150                      155                      160

```

```

Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile Pro Asp
      165                      170                      175

```

```

Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu
      180                      185

```

<210> 23  
 <211> 1251  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
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 gcgccagcag agtcagctgt gccgggcaga tgctggaagt gcagccagga ttgtatttcg 120  
 gtggggccgc ggccgtcgcg gagccagatc acctgagggg agcgggcatc acggccgtgc 180  
 taacagtgga ctccggaggag cccagcttca aggcggggcc tggggtcgag gatctatggc 240  
 gcctcttcgt gccagcgctg gacaaacccg agacggacct actcagccat ctggaccggg 300  
 gcgtggcctt catcggtcag gccgcgctg agggccgtgc ggtgttggtg cactgtcatg 360  
 caggagtcag tcgaagtgtg gccataataa ctgcttttct catgaagact gaccaacttc 420  
 cctttgaaaa agcctatgaa aagctccaga ttctcaaacc agaggctaag atgaatgagg 480  
 ggtttgagt gcaactgaaa ttataccagg caatgggata tgaagtggat acctctagt 540  
 caatttataa gcaatatcgt ttacaaaagg ttacagagaa gtatccagaa ttgcagaatt 600  
 tacctcaaga actctttgct gttgacccaa ctaccgtttc acaaggattg aaagatgagg 660  
 ttctctacaa gtgtagaaag tgcaggcgat cattatttcg aagttctagt attctggatc 720  
 accgtgaagg aagtggacct atagcctttg cccacaagag aatgacacca tcttccatgc 780  
 ttaccacagg gaggcaagct caatgtacat cttatttcat tgaacctgta cagtggatgg 840  
 aatctgcttt gttgggagt atggatggac agcttctttg cccaaaatgc agtgccaagt 900  
 tgggttcctt caactggtat ggtgaacagt gctcttggtg taggtggata acacctgctt 960  
 ttcaaataca taagaataga gtggatgaaa tgaaaatatt gctgttttg ggatcacaaa 1020  
 caggaaaaat atgaacatga tattttatag cttgggaaga aacttgcaga tgatatgtgc 1080  
 tgcctttgct tcttatcatt catggcagat tgtagtgct ttcaacattt catttgaaat 1140  
 gggagaagat aaaatcactt gatgtaacct ggaaactatg ctttacatgg caatcaaagc 1200  
 cttttgatca tgtacatttt atttgatatt aaaatctttt ataaccagaa a 1251

<210> 24  
 <211> 340  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Leu Glu Ala Pro Gly Pro Ser Asp Gly Cys Glu Leu Ser Asn Pro  
 1 5 10 15  
 Ser Ala Ser Arg Val Ser Cys Ala Gly Gln Met Leu Glu Val Gln Pro  
 20 25 30  
 Gly Leu Tyr Phe Gly Gly Ala Ala Ala Val Ala Glu Pro Asp His Leu  
 35 40 45  
 Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Glu Pro  
 50 55 60  
 Ser Phe Lys Ala Gly Pro Gly Val Glu Asp Leu Trp Arg Leu Phe Val  
 65 70 75 80  
 Pro Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg  
 85 90 95  
 Cys Val Ala Phe Ile Gly Gln Ala Arg Ala Glu Gly Arg Ala Val Leu  
 100 105 110  
 Val His Cys His Ala Gly Val Ser Arg Ser Val Ala Ile Ile Thr Ala  
 115 120 125

Phe Leu Met Lys Thr Asp Gln Leu Pro Phe Glu Lys Ala Tyr Glu Lys  
 130 135 140  
 Leu Gln Ile Leu Lys Pro Glu Ala Lys Met Asn Glu Gly Phe Glu Trp  
 145 150 155 160  
 Gln Leu Lys Leu Tyr Gln Ala Met Gly Tyr Glu Val Asp Thr Ser Ser  
 165 170 175  
 Ala Ile Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro  
 180 185 190  
 Glu Leu Gln Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr  
 195 200 205  
 Val Ser Gln Gly Leu Lys Asp Glu Val Leu Tyr Lys Cys Arg Lys Cys  
 210 215 220  
 Arg Arg Ser Leu Phe Arg Ser Ser Ser Ile Leu Asp His Arg Glu Gly  
 225 230 235 240  
 Ser Gly Pro Ile Ala Phe Ala His Lys Arg Met Thr Pro Ser Ser Met  
 245 250 255  
 Leu Thr Thr Gly Arg Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro  
 260 265 270  
 Val Gln Trp Met Glu Ser Ala Leu Leu Gly Val Met Asp Gly Gln Leu  
 275 280 285  
 Leu Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly  
 290 295 300  
 Glu Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His  
 305 310 315 320  
 Lys Asn Arg Val Asp Glu Met Lys Ile Leu Pro Val Leu Gly Ser Gln  
 325 330 335  
 Thr Gly Lys Ile  
 340

&lt;210&gt; 25

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

```

gggcgcctga gccccctata tagatcctca gggcccagaa gcagactctt cggcgggcgcg 60
catgggaccg tcagaagctg ggcgcgcgcg ggcgcgcctcg cccgtaccgc caccgttggt 120
gcgcgtcgcg ccctcactct tcctcgggag cgcgcgagcc gcgggcgcgcg aggagcagct 180
ggcgcgcgcg ggagtcactc tgtgcgtcaa cgtctcccg cagcagcccg gcccgcgcgc 240
gcccggcggtg gcagagctgc gcgtgcccg gttcgacgac ccggtgagg acctgctggc 300
gcacctggag ccacgtgcg ccgccatgga ggccgcggtg cgcgccggcg gcgcctgcct 360
agtctactgc aagaacggcc gcagccagct cggcgccgctc tgcaccgctg acctcatgcg 420
gcaccgcggc ctcagcctgg cgaaggcctt ccagatggtg aagagcgctc gcccggtagc 480

```



agaaccgaac	ccgggcttct	ggtctcagct	ccagaagtat	gaggaggccc	tccaggccca	540
gtcctgcctg	cagggagagc	ccccagcctt	agggttgggc	cctgaggcct	gaagcttgaa	600
ggcctgctgc	ctggaggaag	gatgtccctg	cactgataca	gaaggctggg	ctttaccctt	660
cttcctcact	gtcatatcga	gtttttcc				687

<210> 26

<211> 176

&lt;212&gt; PRT

<213> Homo sapiens

<400> 26

Met Gly Pro Ser Glu Ala Gly Arg Arg Gly Ala Ala Ser Pro Val Pro  
1 5 10 15

Pro Pro Leu Val Arg Val Ala Pro Ser Leu Phe Leu Gly Ser Ala Arg  
20 25 30

Ala Ala Gly Ala Glu Glu Gln Leu Ala Arg Ala Gly Val Thr Leu Cys  
35 40 45

Val Asn Val Ser Arg Gln Gln Pro Gly Pro Arg Ala Pro Gly Val Ala  
50 55 60

Glu Leu Arg Val Pro Val Phe Asp Asp Pro Ala Glu Asp Leu Leu Ala  
65 70 75 80

His Leu Glu Pro Thr Cys Ala Ala Met Glu Ala Ala Val Arg Ala Gly  
85 90 95

Gly Ala Cys Leu Val Tyr Cys Lys Asn Gly Arg Ser Gln Leu Gly Ala  
100 105 110

```
Val Cys Thr Ala Tyr Leu Met Arg His Arg Gly Leu Ser Leu Ala Lys
      115                      120                      125
```

Ala Phe Gln Met Val Lys Ser Ala Arg Pro Val Ala Glu Pro Asn Pro  
130 135 140

Gly Phe Trp Ser Gln Leu Gln Lys Tyr Glu Glu Ala Leu Gln Ala Gln  
145 150 155 160

Ser Cys Leu Gln Gly Glu Pro Pro Ala Leu Gly Leu Gly Pro Glu Ala  
165 170 175

<210> 27

<211> 901

<212> DNA

<213> Homo sapiens

<400> 27

acctgggcaa	taagggaacta	gcagttcagc	cgttttctat	gcctgctgga	tttgtttgta	60
tttgttccca	gccactgctc	atgtaatgta	ctcccttaac	caggaaatta	aagcattctc	120
ccggaataat	ctcaggaagc	aatgcaccag	ggtgacaacg	ctaactggaa	agaaaattat	180
agaaacatgg	aaagatgcca	gaattcatgt	tgtggaagaa	gtagagccga	gcagtggggg	240
tgtgtgtggt	tatgtgcagg	accttagctc	ggacactgca	gttggcgtta	ttaggccatg	300
ggtgtccta	gggtcacaa	atgctgtcta	tgatttggat	acactgaaaa	agaataaggt	360

```

gactcatatt cttaatgttg catatggagt tgaaaatgct ttcctcagtg actttacata 420
taagagcatt tctatattgg atctgcctga aaccaacatc ctgtcttatt ttccagaatg 480
ttttgaattt attgaagaag caaaaagaaa agatggagtg gttcttggtc attgtaatgc 540
aggcgtttcc agggtgctg caattgtaat aggtttcctg atgaattctg aacaaacctc 600
atttaccagt gctttttctt tgggtgaaaaa tgcaagacct tccatatgtc caaattctgg 660
cttcattggag cagcttcgta catatcaaga gggcaaagaa agcaataagt gtgacagaat 720
acaggagaac agttcatgag ttgcattgta gcagacaatg gacaactgta gtttctgaat 780
tgacttctat agccatcttt tccctttttt ggagagtaga ctagcaaaaat tccctttttt 840
ctcttgccctt ttttatgcat aaatggaggt caatctgatt gtcttgacct actgtataaa 900
g

```

```

<210> 28
<211> 217
<212> PRT
<213> Homo sapiens

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<400> 28
Met Tyr Ser Leu Asn Gln Glu Ile Lys Ala Phe Ser Arg Asn Asn Leu
  1             5             10             15

Arg Lys Gln Cys Thr Arg Val Thr Thr Leu Thr Gly Lys Lys Ile Ile
      20             25             30

Glu Thr Trp Lys Asp Ala Arg Ile His Val Val Glu Glu Val Glu Pro
      35             40             45

Ser Ser Gly Gly Gly Cys Gly Tyr Val Gln Asp Leu Ser Ser Asp Leu
      50             55             60

Gln Val Gly Val Ile Lys Pro Trp Leu Leu Leu Gly Ser Gln Asp Ala
      65             70             75             80

Ala His Asp Leu Asp Thr Leu Lys Lys Asn Lys Val Thr His Ile Leu
      85             90             95

Asn Val Ala Tyr Gly Val Glu Asn Ala Phe Leu Ser Asp Phe Thr Tyr
      100            105            110

Lys Ser Ile Ser Ile Leu Asp Leu Pro Glu Thr Asn Ile Leu Ser Tyr
      115            120            125

Phe Pro Glu Cys Phe Glu Phe Ile Glu Glu Ala Lys Arg Lys Asp Gly
      130            135            140

Val Val Leu Val His Cys Asn Ala Gly Val Ser Arg Ala Ala Ala Ile
      145            150            155            160

Val Ile Gly Phe Leu Met Asn Ser Glu Gln Thr Ser Phe Thr Ser Ala
      165            170            175

Phe Ser Leu Val Lys Asn Ala Arg Pro Ser Ile Cys Pro Asn Ser Gly
      180            185            190

Phe Met Glu Gln Leu Arg Thr Tyr Gln Glu Gly Lys Glu Ser Asn Lys
      195            200            205

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Cys Asp Arg Ile Gln Glu Asn Ser Ser  
 210 215

<210> 29  
 <211> 2050  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1954)  
 <223> a, c, g, t, other or unknown

<220>  
 <221> modified\_base  
 <222> (2010)  
 <223> a, c, g, t, other or unknown

<220>  
 <221> modified\_base  
 <222> (2032)  
 <223> a, c, g, t, other or unknown

<400> 29  
 cactataggg cgaattgggc ctctagatgc atgctcgagc ggccgccagt gtgatggata 60  
 tctgcagaat tgcgcccttac gatttaggtg acactataga aggtacgcct gcaggtaccg 120  
 gtccggaatt cccgggtcga cccacgcgtc cgcaatgaag ccgagtgaat gggggctgaa 180  
 tgtcgagtc catagctgaa gaggagcgcc agatgggtgga ggaatacact tatttatgaa 240  
 actgtcttga gttcttcttg aattgccagt ttccagcctc ctcatgcctc cgtctccttt 300  
 agacgacagg gtagtagtgg cactatctag gcccgccga cctcaggatc tcaacctttg 360  
 tttagactct agttaccttg gctctgcca cccaggcagt aacagccacc ctctgtcat 420  
 cgccaccacc gttgtgtccc tcaaggctgc gaatctgacg tatatgcct catccagcgg 480  
 ctctgcccgc tgcgtgaatt gtggatgcag cagtgccagc tgctgcaactg tggcaacct 540  
 cgacaaggac aatcaggccc aaacccaagc cattgccgct ggcaccacca ccaactgccat 600  
 cggaacctct accacctgcc ctgctaacca gatggtcaac aataatgaga atacaggctc 660  
 tctaagtcca tcaagtggg tgggcagccc tgtgtcaggg accccaagc agctagccag 720  
 catcaaaata atctaccca atgacttggc aaagaagatg accaaatgca gcaagagtca 780  
 cctgccgagt cagggccctg tcatcattga ctgcaggccc ttcattggagt acaacaagag 840  
 tcacatccaa ggagctgtcc acattaactg tgccgataag atcagccggc ggagactgca 900  
 gcagggaag atcactgtcc tagacttgat ttctgttagg gaaggcaagg actctttcaa 960  
 gaggatcttt tccaaagaaa ttatagttaa tgatgagaat accaatgagc caagccgagt 1020  
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 <211> 482  
 <212> PRT  
 <213> Homo sapiens

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 Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr  
 35 40 45  
 Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser  
 50 55 60  
 Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys  
 65 70 75 80  
 Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala  
 85 90 95  
 Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys  
 100 105 110  
 Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser  
 115 120 125  
 Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu  
 130 135 140  
 Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr  
 145 150 155 160  
 Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp  
 165 170 175  
 Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val  
 180 185 190  
 His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly  
 195 200 205  
 Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser  
 210 215 220  
 Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr  
 225 230 235 240  
 Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu  
 245 250 255

Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly  
 260 265 270  
 Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu  
 275 280 285  
 Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Gly Ala Ser  
 290 295 300  
 Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala  
 305 310 315 320  
 Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp  
 325 330 335  
 Val Arg Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile  
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 Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe  
 355 360 365  
 Asn Tyr Lys Arg Leu Pro Ser Thr Asp Ser Asn Lys Gln Asn Leu Arg  
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 Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala  
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 Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr  
 420 425 430  
 Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn  
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<210> 31  
 <211> 1026  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
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<210> 32
<211> 341
<212> PRT
<213> Homo sapiens

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Gln Arg Asn Arg Val Thr His Ile Leu Asn Met Ala Arg Glu Ile Asp
      35                      40                      45

Asn Phe Tyr Pro Glu Arg Phe Thr Tyr His Asn Val Arg Leu Trp Asp
      50                      55                      60

Glu Glu Ser Ala Gln Leu Leu Pro His Trp Lys Glu Thr His Arg Phe
      65                      70                      75                      80

Ile Glu Ala Ala Arg Ala Gln Gly Thr His Val Leu Val His Cys Lys
      85                      90                      95

Met Gly Val Ser Arg Ser Ala Ala Thr Val Leu Ala Tyr Ala Met Lys
      100                     105                     110

Gln Tyr Glu Cys Ser Leu Glu Gln Ala Leu Arg His Val Gln Glu Leu
      115                     120                     125

Arg Pro Ile Ala Arg Pro Asn Pro Gly Phe Leu Arg Gln Leu Gln Ile
      130                     135                     140

Tyr Gln Gly Ile Leu Thr Ala Ser Arg Gln Ser His Val Trp Glu Gln
      145                     150                     155                     160

Lys Val Gly Gly Val Ser Pro Glu Glu His Pro Ala Pro Glu Val Ser
      165                     170                     175

Thr Pro Phe Pro Pro Leu Pro Pro Glu Pro Glu Gly Gly Gly Glu Glu
      180                     185                     190

Lys Val Val Gly Met Glu Glu Ser Gln Ala Ala Pro Lys Glu Glu Pro
      195                     200                     205

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 Leu Leu Glu Pro Ser Leu Glu Leu Glu Ser Thr Ser Glu Thr Ser Asp  
 225 230 235 240  
 Met Pro Glu Val Phe Ser Ser His Glu Ser Ser His Glu Glu Pro Leu  
 245 250 255  
 Gln Pro Phe Pro Gln Leu Ala Arg Thr Lys Gly Gly Gln Gln Val Asp  
 260 265 270  
 Arg Gly Pro Gln Pro Ala Leu Lys Ser Arg Gln Ser Val Val Thr Leu  
 275 280 285  
 Gln Gly Ser Ala Val Val Ala Asn Arg Thr Gln Ala Phe Gln Glu Gln  
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 Glu Gln Gly Gln Gly Gln Gly Gln Gly Glu Pro Cys Ile Ser Ser Thr  
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&lt;210&gt; 33

&lt;211&gt; 3995

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

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&lt;210&gt; 34

&lt;211&gt; 777

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

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Met Phe Ser Leu Lys Pro Pro Lys Pro Thr Phe Arg Ser Tyr Phe Leu
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Pro Pro Pro Gln Thr Asp Asp Lys Ile Asn Ser Glu Pro Lys Ile Lys
      20                      25                      30

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Lys Leu Glu Pro Val Leu Leu Pro Gly Glu Ile Val Val Asn Glu Val  
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 Asn Phe Val Arg Lys Cys Ile Ala Thr Asp Thr Ser Gln Tyr Asp Leu  
                   50                                  55                                  60  
 Trp Gly Lys Leu Ile Cys Ser Asn Phe Lys Ile Ser Phe Ile Thr Asp  
                   65                                  70                                  75                                  80  
 Asp Pro Met Pro Leu Gln Lys Phe His Tyr Arg Asn Leu Leu Leu Gly  
                                   85                                  90                                  95  
 Glu His Asp Val Pro Leu Thr Cys Ile Glu Gln Ile Val Thr Val Asn  
                                   100                                  105                                  110  
 Asp His Lys Arg Lys Gln Lys Val Leu Gly Pro Asn Gln Lys Leu Lys  
                                   115                                  120                                  125  
 Phe Asn Pro Thr Glu Leu Ile Ile Tyr Cys Lys Asp Phe Arg Ile Val  
                                   130                                  135                                  140  
 Arg Phe Arg Phe Asp Glu Ser Gly Pro Glu Ser Ala Lys Lys Val Cys  
                                   145                                  150                                  155                                  160  
 Leu Ala Ile Ala His Tyr Ser Gln Pro Thr Asp Leu Gln Leu Leu Phe  
                                   165                                  170                                  175  
 Ala Phe Glu Tyr Val Gly Lys Lys Tyr His Asn Ser Ala Asn Lys Ile  
                                   180                                  185                                  190  
 Asn Gly Ile Pro Ser Gly Asp Gly Gly Gly Gly Gly Gly Gly Gly Asn  
                                   195                                  200                                  205  
 Gly Ala Gly Gly Gly Ser Ser Gln Lys Thr Pro Leu Phe Glu Thr Tyr  
                                   210                                  215                                  220  
 Ser Asp Trp Asp Arg Glu Ile Lys Arg Thr Gly Ala Ser Gly Trp Arg  
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 Val Cys Ser Ile Asn Glu Gly Tyr Met Ile Ser Thr Cys Leu Pro Glu  
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 Tyr Ile Val Val Pro Ser Ser Leu Ala Asp Gln Asp Leu Lys Ile Phe  
                                   260                                  265                                  270  
 Ser His Ser Phe Val Gly Arg Arg Met Pro Leu Trp Cys Trp Ser His  
                                   275                                  280                                  285  
 Ser Asn Gly Ser Ala Leu Val Arg Met Ala Leu Ile Lys Asp Val Leu  
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 Gln Gln Arg Lys Ile Asp Gln Arg Ile Cys Asn Ala Ile Thr Lys Ser  
                                   305                                  310                                  315                                  320  
 His Pro Gln Arg Ser Asp Val Tyr Lys Ser Asp Leu Asp Lys Thr Leu  
                                   325                                  330                                  335

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 580 585 590  
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 Ile Leu Lys Pro Lys Pro Asp Pro Ala Gln Gln Thr Asp Ser Gln Asn  
 610 615 620  
 Ser Asp Thr Glu Gln Tyr Phe Arg Glu Trp Phe Ser Lys Pro Ala Asn  
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Leu His Gly Val Ile Leu Pro Arg Val Ser Gly Thr His Ile Lys Leu  
                     645                    650                    655  
 Trp Lys Leu Cys Tyr Phe Arg Trp Val Pro Glu Ala Gln Ile Ser Leu  
                     660                    665                    670  
 Gly Gly Ser Ile Thr Ala Phe His Lys Leu Ser Leu Leu Ala Asp Glu  
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 Val Asp Val Leu Ser Arg Met Leu Arg Gln Gln Arg Ser Gly Pro Leu  
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 Glu Ala Cys Tyr Gly Glu Leu Gly Gln Ser Arg Met Tyr Phe Asn Ala  
                     705                    710                    715                    720  
 Ser Gly Pro His His Thr Asp Thr Ser Gly Thr Pro Glu Phe Leu Ser  
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 Ser Ser Phe Pro Phe Ser Pro Val Gly Asn Leu Cys Arg Arg Ser Ile  
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 Leu Gly Thr Pro Leu Ser Lys Phe Leu Ser Gly Ala Lys Ile Trp Leu  
                     755                    760                    765  
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&lt;210&gt; 35

&lt;211&gt; 2353

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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tgagtgtgtt tggcagttaa tggaacaatt tccctgtgcc tttgagttca atgagaggtt 1500
tttgattcac attcaacatc acattttattc ctgccagttt ggaaacttcc tatgtaacag 1560
ccaaaaggag agacgagaac tcaagattca agaaagaaca tactcattat gggctcacct 1620
gtggaagaat cgggcccact acctgaatcc tctgtttaga gctgatcaca gccagactca 1680
gggaaccttt catctcccta caacaccatg taacttcatg tacaagtttt ggagtggaa 1740
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agtgaaggaa gaaactcagc agctagagga agaactagag gccctggaag aagtaagaca 1860
tacttgcttt gttaatctat tttctgtgct tatttcttga agagcaaggc ttcataaag 1920
cctcttaaga ttcagtgcac tacaatatatt tcacattttt agtcagtaga acacctgaaa 1980
cacaacccca tccaggtcag gactcagata accgaagccc aaacctaggc atttaatgca 2040
tttcacacat ctggtttgtg gctcagttcc acaaattttt gggtgttcct tatttttaggt 2100
caacttggtt gggtactgtt atttgagagt agtaaaatta atttttttct ggaaagtgtg 2160
aaaaagtaac agaataaaaat caaatatatg tacttgtaaa actctttccc cacttttaga 2220
aattatgtta actatgatat taatctataa ttggtaaagg ggagactgac tgtaaagtct 2280
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ttcctaattg gaa 2353

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<210> 36  
 <211> 629  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Met Val Pro Pro Lys Leu Gln Glu Ala Phe Glu Pro Phe Asp Leu Lys  
 1 5 10 15  
 His Ala Gly Ala His Phe Arg Ala Pro Pro Arg Glu Ser Leu Asp His  
 20 25 30  
 Arg Glu Asn Arg Val Phe Arg Gly Phe Ala Pro Pro Asp Lys Arg Asn  
 35 40 45  
 Glu Gln Ala Gly Ser Ser Ser Ala Val Val Ser Val Phe Tyr Val Cys  
 50 55 60  
 Gly Met Ala Gln Tyr Ser Ser Ser Ser Ser Val Ala Gln Gly Ser  
 65 70 75 80  
 Arg Lys Val Glu Asn Val Arg Leu Val Asp Arg Val Ser Pro Lys Lys  
 85 90 95  
 Ala Ala Leu Gly Thr Leu Tyr Leu Thr Ala Thr His Val Ile Phe Val  
 100 105 110  
 Glu Asn Ser Pro Asp Ala Arg Lys Glu Thr Trp Ile Leu His Ser Gln  
 115 120 125  
 Ile Ser Thr Ile Glu Lys Gln Ala Thr Thr Ala Thr Gly Cys Pro Leu  
 130 135 140  
 Leu Ile Arg Cys Lys Asn Phe Gln Ile Ile Gln Leu Ile Ile Pro Gln  
 145 150 155 160  
 Glu Arg Asp Cys His Asp Val Tyr Ile Ser Leu Ile Arg Leu Ala Arg  
 165 170 175

Pro Val Lys Tyr Glu Glu Leu Tyr Cys Phe Ser Phe Asn Pro Met Leu  
 180 185 190  
 Asp Lys Glu Glu Arg Glu Gln Gly Trp Val Leu Ile Asp Leu Ser Glu  
 195 200 205  
 Glu Tyr Thr Arg Met Gly Leu Pro Asn His Tyr Trp Gln Leu Ser Asp  
 210 215 220  
 Val Asn Arg Asp Tyr Arg Val Cys Asp Ser Tyr Pro Thr Glu Leu Tyr  
 225 230 235 240  
 Val Pro Lys Ser Ala Thr Ala His Ile Ile Val Gly Ser Ser Lys Phe  
 245 250 255  
 Arg Ser Arg Arg Arg Phe Pro Val Leu Ser Tyr Tyr Tyr Lys Asp Asn  
 260 265 270  
 His Ala Ser Ile Cys Arg Ser Ser Gln Pro Leu Ser Gly Phe Ser Ala  
 275 280 285  
 Arg Cys Leu Glu Asp Glu Gln Met Leu Gln Ala Ile Arg Lys Ala Asn  
 290 295 300  
 Pro Gly Ser Asp Phe Val Tyr Val Val Asp Thr Arg Pro Lys Leu Asn  
 305 310 315 320  
 Ala Met Ala Asn Arg Ala Ala Gly Lys Gly Tyr Glu Asn Glu Asp Asn  
 325 330 335  
 Tyr Ser Asn Ile Lys Phe Gln Phe Ile Gly Ile Glu Asn Ile His Val  
 340 345 350  
 Met Arg Asn Ser Leu Gln Lys Met Leu Glu Val Cys Glu Leu Lys Ser  
 355 360 365  
 Pro Ser Met Ser Asp Phe Leu Trp Gly Leu Glu Asn Ser Gly Trp Leu  
 370 375 380  
 Arg His Ile Lys Ala Ile Met Asp Ala Gly Ile Phe Ile Ala Lys Ala  
 385 390 395 400  
 Val Ser Glu Glu Gly Ala Ser Val Leu Val His Cys Ser Asp Gly Trp  
 405 410 415  
 Asp Arg Thr Ala Gln Val Cys Ser Val Ala Ser Leu Leu Leu Asp Pro  
 420 425 430  
 His Tyr Arg Thr Leu Lys Gly Phe Met Val Leu Ile Glu Lys Asp Trp  
 435 440 445  
 Ile Ser Phe Gly His Lys Phe Asn His Arg Tyr Gly Asn Leu Asp Gly  
 450 455 460  
 Asp Pro Lys Glu Ile Ser Pro Val Ile Asp Gln Phe Ile Glu Cys Val  
 465 470 475 480

Trp Gln Leu Met Glu Gln Phe Pro Cys Ala Phe Glu Phe Asn Glu Arg  
 485 490 495  
 Phe Leu Ile His Ile Gln His His Ile Tyr Ser Cys Gln Phe Gly Asn  
 500 505 510  
 Phe Leu Cys Asn Ser Gln Lys Glu Arg Arg Glu Leu Lys Ile Gln Glu  
 515 520 525  
 Arg Thr Tyr Ser Leu Trp Ala His Leu Trp Lys Asn Arg Ala Asp Tyr  
 530 535 540  
 Leu Asn Pro Leu Phe Arg Ala Asp His Ser Gln Thr Gln Gly Thr Phe  
 545 550 555 560  
 His Leu Pro Thr Thr Pro Cys Asn Phe Met Tyr Lys Phe Trp Ser Gly  
 565 570 575  
 Met Tyr Asn Arg Phe Glu Lys Gly Met Gln Pro Arg Gln Ser Val Thr  
 580 585 590  
 Asp Tyr Leu Met Ala Val Lys Glu Glu Thr Gln Gln Leu Glu Glu Glu  
 595 600 605  
 Leu Glu Ala Leu Glu Glu Val Arg His Thr Cys Phe Val Asn Leu Phe  
 610 615 620  
 Ser Val Leu Ile Ser  
 625

&lt;210&gt; 37

&lt;211&gt; 1200

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

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gacagtccac agacaaacga atttaaagga gcaaccgagg aggcacctgc gaaagaaagc 120
ccacacacaa gtgaatttaa aggagcagcc ctggtgtcac ctatcagtaa aagtatgtta 180
gaacgacttt ccaagtttga agttgaagat gctgaaaatg ttgcttcata tgacagcaag 240
attaagaaaa ttgtgcattc aattgtatca tcctttgcat ttggactatt tggagttttc 300
ctggtcttac tggatgtcac tctcgctctt gccgacctaa ttttactga cagcaaactt 360
tatattcctt cggagtatcg ttctatttct ctagctattg ccttattttt tctcatggat 420
gttcttcttc gagtatttgt agaagggccc gtctatacca ttgggctgcc cccttcagac 480
ctccgggcag gaaaagaaga gactgtactg gtcagagaaa gacatcagca ggagagccag 540
agattcctcc tcctctccat catcaccatc accattattc tcatcaccat caccgtcacc 600
gtcatcaaat attttaattt aactaaaaat attaaacttg aaatcagtaa gatggtggta 660
ttctccaagg aagtaaataa gtggatgact caagatcctg aaaacatcat agtgattcac 720
tgtaaaggag gcaaaatcat catcaccatc atggacttca aagaagtttg tacaactcaa 780
tattgcaaag ttgtcagttc tctcaagtta atctataaat tcaatgtagt tccaataaaa 840
atcctaaatg tgaaaggaag aaccggaact atggtttgtg cgctccttat tgccctcgaa 900
atatttttaa ctgcagagga aagcctgtat tattttggag aaaggcgaac agataaaacc 960
cacagcaata aatttcaggg agtagaaaact ccttgtcaga atagatatgt tggatatattt 1020
gcacaagtga aacatctcta caacgggaat atccctccaa gacggatact ctttataaaa 1080
agattcatta ttattcgac tcgtggtggt ggaacaggtg atgtatgtga tctacaattc 1140
caaatagtaa tggagaaaaa gggtgtcttt tccagtactt cattaggaaa ttgttcgctg 1200

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<210> 38  
 <211> 400  
 <212> PRT  
 <213> Homo sapiens

<400> 38

Met	Asn	Glu	Ser	Pro	Asp	Pro	Asn	Ala	Leu	Ala	Gly	Val	Ile	Ile	Glu	1	5	10	15
Arg	Ala	Pro	Ser	Asp	Ser	Pro	Gln	Thr	Asn	Glu	Phe	Lys	Gly	Ala	Thr	20	25	30	
Glu	Glu	Ala	Pro	Ala	Lys	Glu	Ser	Pro	His	Thr	Ser	Glu	Phe	Lys	Gly	35	40	45	
Ala	Ala	Leu	Val	Ser	Pro	Ile	Ser	Lys	Ser	Met	Leu	Glu	Arg	Leu	Ser	50	55	60	
Lys	Phe	Glu	Val	Glu	Asp	Ala	Glu	Asn	Val	Ala	Ser	Tyr	Asp	Ser	Lys	65	70	75	80
Ile	Lys	Lys	Ile	Val	His	Ser	Ile	Val	Ser	Ser	Phe	Ala	Phe	Gly	Leu	85	90	95	
Phe	Gly	Val	Phe	Leu	Val	Leu	Leu	Asp	Val	Thr	Leu	Val	Leu	Ala	Asp	100	105	110	
Leu	Ile	Phe	Thr	Asp	Ser	Lys	Leu	Tyr	Ile	Pro	Ser	Glu	Tyr	Arg	Ser	115	120	125	
Ile	Ser	Leu	Ala	Ile	Ala	Leu	Phe	Phe	Leu	Met	Asp	Val	Leu	Leu	Arg	130	135	140	
Val	Phe	Val	Glu	Gly	Pro	Val	Tyr	Thr	Ile	Gly	Leu	Pro	Pro	Ser	Asp	145	150	155	160
Leu	Arg	Ala	Gly	Lys	Glu	Glu	Thr	Val	Leu	Val	Arg	Glu	Arg	His	Gln	165	170	175	
Gln	Glu	Ser	Gln	Arg	Phe	Leu	Leu	Leu	Ser	Ile	Ile	Thr	Ile	Thr	Ile	180	185	190	
Ile	Leu	Ile	Thr	Ile	Thr	Val	Thr	Val	Ile	Lys	Tyr	Phe	Asn	Leu	Thr	195	200	205	
Lys	Asn	Ile	Lys	Leu	Glu	Ile	Ser	Lys	Met	Val	Val	Phe	Ser	Lys	Glu	210	215	220	
Val	Asn	Glu	Trp	Met	Thr	Gln	Asp	Pro	Glu	Asn	Ile	Ile	Val	Ile	His	225	230	235	240
Cys	Lys	Gly	Gly	Lys	Ile	Ile	Ile	Thr	Ile	Met	Asp	Phe	Lys	Glu	Val	245	250	255	
Cys	Thr	Thr	Gln	Tyr	Cys	Lys	Val	Val	Ser	Ser	Leu	Lys	Leu	Ile	Tyr	260	265	270	

Lys Phe Asn Val Val Pro Ile Lys Ile Leu Asn Val Lys Gly Arg Thr  
 275 280 285  
 Gly Thr Met Val Cys Ala Leu Leu Ile Ala Ser Glu Ile Phe Leu Thr  
 290 295 300  
 Ala Glu Glu Ser Leu Tyr Tyr Phe Gly Glu Arg Arg Thr Asp Lys Thr  
 305 310 315 320  
 His Ser Asn Lys Phe Gln Gly Val Glu Thr Pro Cys Gln Asn Arg Tyr  
 325 330 335  
 Val Gly Tyr Phe Ala Gln Val Lys His Leu Tyr Asn Gly Asn Ile Pro  
 340 345 350  
 Pro Arg Arg Ile Leu Phe Ile Lys Arg Phe Ile Ile Tyr Ser Thr Arg  
 355 360 365  
 Gly Val Gly Thr Gly Asp Val Cys Asp Leu Gln Phe Gln Ile Val Met  
 370 375 380  
 Glu Lys Lys Val Val Phe Ser Ser Thr Ser Leu Gly Asn Cys Ser Leu  
 385 390 395 400

<210> 39  
 <211> 694  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
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 gttcctgttg gacctgggcg tgcggcacct ggtgtccctg acggagcgcg ggccccctca 180  
 cagcgacagc tgccccggcc tcaccctgca ccgcctgcgc atccccgact tctgccccgcc 240  
 ggcccccgac cagatcgacc gcttcgtgca gatcgtggac gaggccaacg cacggggaga 300  
 ggctgtggga gtgcaactgt ctctgggctt tggccgcact ggcaccatgc tggcctgtta 360  
 cctggtgaag gagcggggct tggctgcagg agatgccatt gctgaaatcc gacgactacg 420  
 acccgggccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480  
 gaaataaggg gccttagtac ctttctacca ggccctcact ccccttcccc atgttgctga 540  
 tggggccaga gatgaaggga agtggactaa agtattaaac cctctagctc ccattggctg 600  
 aagacactga agtagccac ccctgcaggc aggtcctgat tgaaggggag gcttgtactg 660  
 ctttgttgaa taaatgagtt ttacgaacca ggga 694

<210> 40  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
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 Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu  
 20 25 30



Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro  
           35                          40                          45  
 His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro  
           50                          55                          60  
 Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile  
           65                          70                          75                          80  
 Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala  
                           85                          90                          95  
 Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys  
                           100                          105                          110  
 Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu  
           115                          120                          125  
 Arg Pro Gly Pro Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln  
           130                          135                          140  
 Phe Tyr Gln Arg Thr Lys  
           145                          150

<210> 41  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<220>  
 <221> modified\_base  
 <222> (57)  
 <223> a, c, g, t, other or unknown

<400> 41  
 aagcagtgggt aacaacgcag agtactttttt tttttttttt tttttttttt tttttvn 57

<210> 42  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 42  
 aagtggcaac agagataacg cgtacgcggg 30

<210> 43  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 43

aagcagtggg aacaacgcag agtacgcggg

30

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 44

aagcagtggg aacaacgcag agt

23

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 45

aagtggcaac agagataacg cgt

23